



SEQUENCE LISTING

C/ <110> Astra Aliebolag

<120> Vaccine Delivery System and Method of Production

<130> 1103326-0560

<140> 09/308,435

<141> 1999-05-19

<150> PCT/SE99/00582

<151> 1999-04-09

<150> SE 9801288-3

<151> 1998-04-14

<160> 25

<170> PatentIn Ver. 2.1

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<211> 1670

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (793)..(1572)

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gatttgattt taggaaatta catgcaagtg aatgaaaaaa acattcaagc gtttgc(cc)cc 180

aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaatcaa cctaaaatgg 240

tggatatagg ggataaagaa accactgaaa gaatcgctct agcaagcggt cgtatcagca 300

tgaataaaga ggcttatgac gctattatca atcatggcgt caaaaagggt ccggtattac 360

aaactgctat tattgctggg attatggggg ctaaaaagac aagcgactc attccatgt 420

gccatccaat catgctcaat ggggtggata ttgatattt agaagaaaaa gagacttgta 480

gttttaact ctagcgaga gtcaaaactc aagctaaaac gggcgtagaa atggaagcgc 540

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TECH CENTER 1600/2900

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   Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu  
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Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys			
210	215	220	
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Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys			
225	230	235	
aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa		1551	
Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu			
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Leu Lys Gly Lys Arg Asn Arg			
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20	25	30	
Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser			
35	40	45	
Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala			
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Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys			
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Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr			
85	90	95	
Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala			
100	105	110	

Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val  
 115 120 125  
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 130 135 140  
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 145 150 155 160  
 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser  
 165 170 175  
 Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys  
 180 185 190  
 Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr  
 195 200 205  
 Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu  
 210 215 220  
 Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr  
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<220>  
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 gatttgattt taggaaatta catgcaagtg aatgaaaaaa acattcaagc gtttgc(cc)cc 180  
 aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaaatcaa cctaaaatgg 240  
 tggatataagg ggataaaagaa accactgaaa gaatcgctct agcaagcggc cgtatcagca 300

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   Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser  
   15                  20                  25

ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat   927  
   Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His  
   30                  35                  40                  45

cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta   975  
   Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu  
   50                  55                  60

agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac   1023  
   Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn  
   65                  70                  75

aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat   1071  
   Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn  
   80                  85                  90

caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt   1119  
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   95                  100                  105

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   130                  135                  140

gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt 1263  
 Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val  
 145 150 155

tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt 1311  
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 160 165 170

ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att 1359  
 Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile  
 175 180 185

caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta 1407  
 Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu  
 190 195 200 205

gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag 1455  
 Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys  
 210 215 220

aga gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa 1503  
 Arg Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys  
 225 230 235

aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa 1551  
 Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu  
 240 245 250

tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg 1602  
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Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser  
 35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala  
 50 55 60

Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys  
 65 70 75 80

Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr  
 85 90 95

Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala  
 100 105 110

Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val  
 115 120 125

Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly  
 130 135 140

Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro  
 145 150 155 160

Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser  
 165 170 175

Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys  
 180 185 190

Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr  
 195 200 205

Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu  
 210 215 220

Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr  
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Lys Arg Asn Arg  
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Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu			
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20	25	30	
Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser			
35	40	45	
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Leu Gly Ala Ser Val Gly Ala Leu Leu Val Gly Cys Ser Pro His Ile			
20	25	30	
Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser			
35	40	45	
Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu			
50	55	60	
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Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile  
20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser  
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu  
50 55 60

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<213> Helicobacter pylori

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20 25 30

Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser  
35 40 45

Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu  
50 55 60

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35 40 45

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Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser Asp Lys Asp Asp  
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Ala Ser Ile Met Gln Glu Met Asp Lys Lys Leu Thr  
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20 25 30  
  
Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe  
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35 40 45  
  
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Lys Arg Asn Arg  
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Lys Arg Asn Arg  
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20 25 30

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<220>  
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cysteine residue at position 31

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Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Leu Ala Gly Cys  
20 25 30

<210> 25  
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<212> PRT  
<213> Helicobacter pylori

<220>  
<221> MOD\_RES  
<222> (31)

<223> lipid chains a and b attached respectively at  
positions 3 and 2 of propyl group attached to  
sulphydryl of cysteine residue at position 31

<400> 25

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1 5 10 15

Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Leu Ala Gly Cys  
20 25 30

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